



09913064.080802

#66

SEQUENCE LISTING

<110> Carlson, Thomas J.
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Pearlstein, Richard W.
Rafalski, J. Antoni
Thorpe, Catherine J.

<120> UDP-Glucose Modifiers

<130> BB-1321-1

<140> 09/913,064

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<151> 2000-02-09

<150> 60/119,588

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20 25 30

Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Val Ile Gly Thr
35 40 45

Ile Asn Leu Leu Glu Val Met Ser Val His Gly Cys Lys Lys Leu Val
50 55 60

Phe Ser Ser Ser Ala Ala Val Tyr Gly Ser Pro Lys Asn Ser Pro Cys
65 70 75 80

Thr Glu Asn Phe Pro Leu Thr Pro Asn Asn Pro Tyr Gly Lys Thr Lys
85 90 95

Leu Val Val Glu Asp Ile Cys Arg Asp Ile Tyr Arg Ser Asp Pro Glu
100 105 110

Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro
115 120 125

Ser Gly Tyr Leu Gly Glu Asp Pro Arg Xaa Ile Pro Asn Asn Leu Met
130 135 140

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 35 40 45
 Gly His Asn Ala Asn Asn Leu Asp Phe Arg Lys Gly Asp Leu Arg Asp
 50 55 60
 Lys Gln Ala Leu Xaa Gln Ile Phe Ser Ser Gln Lys Val Glu Xaa Val
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 gtgggtggnc ctctgcttct tcaaaaacct caattcaccc aaggngatct ccggaatagg 240
 gatgacttgg agaaactctt ctccaaaaca acatttgatg ccgtgatcca ctttgcctggc 300
 ttgaaaagcy gttgctgaaa gcgtttgcgaa acccgcgtgc tattttgatt ttaatttggn 360
 tgggaccanc aacctctacg agtttatggn aaagtataat tgcaaaaaga tgggtttctc 420
 atcatctgca accgtttatg ggcaanctga aaaaataccg tgtgaggagg attcaagtt 479

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 Ile Gly Thr His Thr Val Val Xaa Leu Leu Lys Ala Gly Phe Ser Val
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 Ser Ile Ile Asp Asn Phe Asp Asn Ser Val Met Glu Ala Met Asp Arg
 35 40 45
 Val Arg Gln Val Val Gly Pro Leu Leu Ser Gln Asn Leu Gln Phe Thr
 50 55 60
 Gln Gly Asp Leu Arg Asn Arg Asp Asp Leu Glu Lys Leu Phe Ser Lys
 65 70 75 80
 Thr Thr Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Ala
 85 90 95
 Glu Ser Val Ala Lys Pro Arg Arg Tyr Phe Asp Phe Asn Leu Xaa Gly
 100 105 110
 Thr Xaa Asn Leu Tyr Glu Phe Met Xaa Lys Tyr Asn Cys Lys Lys Met
 115 120 125
 Gly Phe Ser Ser Ser Ala Thr Val Tyr Gly Gln Xaa Glu Lys Ile Pro
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 Cys Glu Glu Asp
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 <213> Triticum aestivum

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 Gln Leu Leu Glu Lys Gly Tyr Ala Val Thr Ala Val Asp Asn Phe His
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 35 40 45
 Ala Leu Ser Ala Arg Leu Gln Phe Ile Phe Gly Asp Leu Thr Ile Lys
 50 55 60
 Asp Asp Leu Glu Lys Val Phe Ala Ala Lys Lys Tyr Asp Ala Val Ile
 65 70 75 80
 His Phe Ala Gly Leu Lys Ala Val Ala Glu Ser Val Ala His Pro Glu
 85 90 95
 Met Tyr Asn Arg Asn Asn Ile Val Gly Thr Val Asn Leu Tyr Asp Val
 100 105 110

Met Lys Lys His Gly Cys Asn Lys Leu Val Phe Ser Ser Ser Ala Thr
 115 120 125

Val Tyr Gly Gln Pro Glu Lys Val Pro Cys Phe Glu Asp Ser Pro Leu
 130 135 140

Lys Ala Leu Asn Pro Tyr Gly Arg Thr Lys Leu Tyr Trp Arg Arg Ser
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Ala Arg

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Ala	His	Pro	Glu	Met	Tyr	Tyr	Glu	Asn	Asn	Leu	Ile	Gly	Thr	Ile	Asn
			20					25					30		

Leu	Tyr	Lys	Ser	Met	Lys	Glu	His	Gly	Cys	Lys	Lys	Leu	Val	Phe	Ser
	35						40					45			

Ser	Ser	Ala	Thr	Val	Tyr	Gly	Trp	Pro	Glu	Val	Ile	Pro	Cys	Val	Glu
	50					55					60				

Asp	Ser	Lys	Leu	Gln	Ala	Ala	Asn	Pro	Tyr	Gly	Arg	Thr	Lys	Leu	Ile
65				70					75					80	

Leu	Glu	Asp	Met	Ala	Arg	Asp	Tyr	His	Arg	Ala	Asp	Thr	Glu	Trp	Ser
			85						90					95	

Ile	Val	Leu	Leu	Arg	Tyr	Phe	Asn	Pro	Ile	Gly	Ala	His	Ser	Ser	Gly
		100					105						110		

Xaa	Ile	Xaa	Arg	Gly	Pro	Gln	Gly	Asp	Thr	Glu	Gln	Pro	Ala	Ala	Leu
	115					120					125				

His	Pro	Ala	Gly	Xaa	Arg	Arg	Xaa	Ala	Pro	Arg	Ala	Gln	Arg	Leu	Arg
	130					135					140				

Xaa	Thr	Ile	Thr	Pro	Pro	Gly	Asp	Gly	Thr	Ala	Ile	Arg	Asp	Tyr	Ile
145				150					155					160	

His	Val	Val	Glu	Leu	Ala	Asp	Gly	His	Ile	Ala	Arg	Ala	Xaa	Glu	Leu
			165					170						175	

Xaa	Asp	Ser	Pro	Asp	Ile	Ser	Cys	Val	Gly	Tyr	Asn	Leu	Gly	Val	Gln
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Gly	Arg	Arg	Xaa	Xaa	
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 agagatagtg gttctcgtcg tnggcgaacg tgtncggcca gccgganaag accccctgcg 240
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Tyr Asp Ala Val Ile His Phe Ala Gly Leu Lys Xaa Trp Gly Arg Ala
20 25 30

Ser Arg Asn Pro Gln Met Tyr Tyr Glu Asp Asn Val Ala Gly Thr Met
35 40 45

Asn Leu Xaa Ser Ala Leu Thr Lys Tyr Gly Xaa Xaa Xaa Ile Val Phe
50 55 60

Ser Ser Xaa Ala Thr Val Xaa Gly Gln Pro Xaa Lys Thr Pro Cys Val
65 70 75 80

Glu Xaa Ser Xaa Leu Ser Ala Leu Asn Pro Tyr Gly Ala Xaa Xaa Leu
85 90 95

Val Leu Glu

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gatatctcaga	aagctgaacc	agaatgggaag	atcatattac	tgagataact	caatccagtt	600
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tctggcaaga	aaattccagt	aaaattatgt	ccaagaagac	cgggagatgc	gactgaggtt	960
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tctcttatat	agaatacttt	tatgtttgat	gatttgttta	ggcagttcgt	tgataaatct	1200
tgacaataaa	aatttggcag	catttcaaga	agttaaagct	atgtatttta	acaataaact	1260
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<212> PRT

<213> Glycine max

<400> 14

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Ile Gly Thr His Thr Val Val Gln Leu Lys Ala Gly Phe Ser Val
          20           25           30

Ser Ile Ile Asp Asn Phe Asp Asn Ser Val Met Glu Ala Val Asp Arg
          35           40           45

Val Arg Gln Val Val Gly Pro Leu Leu Ser Gln Asn Leu Gln Phe Thr
          50           55           60

Gln Gly Asp Leu Arg Asn Arg Asp Asp Leu Glu Lys Leu Phe Ser Lys
          65           70           75           80

Thr Thr Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Ala
          85           90           95

Glu Ser Val Ala Lys Pro Arg Arg Tyr Phe Asp Phe Asn Leu Val Gly
          100          105          110

Thr Ile Asn Leu Tyr Glu Phe Met Ala Lys Tyr Asn Cys Lys Lys Met
          115          120          125

Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Lys Ile Pro
          130          135          140

Cys Glu Glu Asp Phe Lys Leu Gln Ala Met Asn Pro Tyr Gly Arg Thr
          145          150          155          160

Lys Leu Phe Leu Glu Glu Ile Ala Arg Asp Ile Gln Lys Ala Glu Pro
          165          170          175

Glu Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His
          180          185          190

Glu Ser Gly Lys Leu Gly Glu Asp Pro Lys Gly Ile Pro Asn Asn Leu
          195          200          205

Met Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Thr Glu Leu Asn
          210          215          220

Val Tyr Gly His Asp Tyr Pro Thr Arg Asp Gly Ser Ala Ile Arg Asp
          225          230          235          240

Tyr Ile His Val Met Asp Leu Ala Asp Gly His Ile Ala Ala Leu Arg
          245          250          255

Lys Leu Phe Thr Thr Glu Asn Ile Gly Cys Thr Ala Tyr Asn Leu Gly
          260          265          270

Thr Gly Arg Gly Thr Ser Val Leu Glu Met Val Thr Ala Phe Glu Lys
          275          280          285

Ala Ser Gly Lys Lys Ile Pro Val Lys Leu Cys Pro Arg Arg Pro Gly
          290          295          300

Asp Ala Thr Glu Val Tyr Ala Ser Thr Glu Arg Ala Glu Lys Glu Leu

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305

310

315

320

Gly Trp Lys Ala Asn Tyr Gly Val Glu Glu Met Cys Arg Asp Gln Trp
 325 330 335

Asn Trp Ala Lys Asn Asn Pro Trp Gly Tyr Ala Gly Lys Pro
 340 345 350

<210> 15

<211> 1516

<212> DNA

<213> Triticum aestivum

<220>

<221> unsure

<222> (1458)..(1459)

<223> n = A, C, G, OR T

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 gacgcgctga tacacttcgc cgggctcaag gcggtggcgg agagcgtggc gcaccgggag 300
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 ggggtgcaaca agttggtggt ctgcgtcgct gcgaccgtgt acggccagacc ggagaagggtg 420
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<210> 16

<211> 352

<212> PRT

<213> Triticum aestivum

<400> 16

Ala Arg Gly Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile Gly Thr
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His Thr Val Leu Gln Leu Leu Glu Lys Gly Tyr Ala Val Thr Ala Val
 20 25 30

Asp Asn Phe His Asn Ser Val Pro Glu Ala Leu Asp Arg Val Arg His
 35 40 45

Ile Val Gly Pro Ala Leu Ser Ala Arg Leu Gln Phe Ile Phe Gly Asp
 50 55 60
 Leu Thr Ile Lys Asp Asp Leu Glu Lys Val Phe Ala Ala Lys Lys Tyr
 65 70 75 80
 Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Ala Glu Ser Val
 85 90 95
 Ala His Pro Glu Met Tyr Asn Arg Asn Asn Ile Val Gly Thr Val Asn
 100 105 110
 Leu Tyr Asp Val Met Lys Lys His Gly Cys Asn Lys Leu Val Phe Ser
 115 120 125
 Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Lys Val Pro Cys Phe Glu
 130 135 140
 Asp Ser Pro Leu Lys Ala Leu Asn Pro Tyr Gly Arg Thr Lys Leu Tyr
 145 150 155 160
 Leu Glu Glu Met Leu Arg Asp Tyr Gln His Ala Asn Pro Glu Trp Arg
 165 170 175
 Thr Ile Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Glu Ser Gly
 180 185 190
 Asp Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu Pro Tyr
 195 200 205
 Ile Gln Gln Val Ala Val Ala Arg Arg Pro Glu Leu Asn Val Tyr Gly
 210 215 220
 His Asp Tyr Arg Thr Arg Asp Gly Thr Ala Val Arg Asp Tyr Ile His
 225 230 235 240
 Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Glu Lys Leu Phe
 245 250 255
 Ala Thr Pro Asp Ile Gly Cys Val Ala Tyr Asn Leu Gly Thr Gly Arg
 260 265 270
 Gly Thr Thr Val Leu Glu Met Val Ser Ala Phe Glu Lys Ala Tyr Gly
 275 280 285
 Lys Lys Ile Pro Val Lys Met Cys Pro Arg Arg Pro Gly Asp Ser Glu
 290 295 300
 Gln Val Tyr Ala Ser Thr Ala Lys Ala Glu Glu Glu Leu Gly Trp Arg
 305 310 315 320
 Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala
 325 330 335
 Lys Lys Asn Pro Tyr Gly Tyr Cys Gly Asn Ala Ala Glu Asn Lys Asp
 340 345 350

<210> 17
 <211> 1393
 <212> DNA
 <213> Zea mays


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<400> 17
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tactttatta tgacaacaac gtcattggca cgataaatct tctagaagtt atgtctgttc 180
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cacccctgcac agaaaaatttt cctcttactc caaacaatcc atatggcaaa acaagctcg 300
ttgttgaga tatttgcggg gatactacc gttcagatcc tgaatggagat acattttac 360
ttaggtactt caatccagtt ggtgctcatc ctagtggata tcttggcgag gacccacgag 420
gaattcccaa caatccttat cctatgttc agcaagttgc ggttggtagg agccagctc 480
taacagtttt aggaatgac tatgcaacaa gagatgggac tggggtcoga gattacatcc 540
atgtggttga ccttgcgtgac ggacatatgt ctgcattgca gaagcttttt gagaactcta 600
gcatagggtg tgaagcgtae aaccttggaa cgggaagagg tacatctgtg ctggagattg 660
ttaaagcatt tgagaagcct tctgggaaga aaatacctct gatttttggg gaaagacgcc 720
caggtgatgc agagattctg ttttcagaga ctactaaagc agagagggag cttaactgga 780
aagcaaaata cggatttgaa gagatgtgcc gcgaccaatg gaactgggcc agcaagaacc 840
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ctgactcctc caagcagaat ggccacgcga caaacggctc aactgactca cccaagcgga 960
acggccacca tgcgtatggg tctgctgact cacccaagcg caacggggcac tgcgtttttg 1020
gatcatcaga cctcaagccg aatggtaatt gccacctgcg ctgacgagaa ctgtttggcc 1080
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aaaaaaaaaaa aaa 1393

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<210> 18
<211> 353
<212> PRT
<213> Zea mays

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<400> 18
Thr Arg Ile Asp Leu Arg Asp Lys Gly Ala Leu Glu Met Val Phe Ala
1 5 10 15

Ser Thr Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys Ala Val
20 25 30

Gly Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Val Ile
35 40 45

Gly Thr Ile Asn Leu Leu Glu Val Met Ser Val His Gly Cys Lys Lys
50 55 60

Leu Val Phe Ser Ser Ser Ala Ala Val Tyr Gly Ser Pro Lys Asn Ser
65 70 75 80

Pro Cys Thr Glu Asn Phe Pro Leu Thr Pro Asn Asn Pro Tyr Gly Lys
85 90 95

Thr Lys Leu Val Val Glu Asp Ile Cys Arg Asp Ile Tyr Arg Ser Asp
100 105 110

Pro Glu Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala
115 120 125

His Pro Ser Gly Tyr Leu Gly Glu Asp Pro Arg Gly Ile Pro Asn Asn
130 135 140

Leu Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro Ala Leu

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145 150 155 160

Thr Val Leu Gly Asn Asp Tyr Ala Thr Arg Asp Gly Thr Gly Val Arg
165 170 175

Asp Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu
180 185 190

Gln Lys Leu Phe Glu Asn Ser Ser Ile Gly Cys Glu Ala Tyr Asn Leu
195 200 205

Gly Thr Gly Arg Gly Thr Ser Val Leu Glu Ile Val Lys Ala Phe Glu
210 215 220

Lys Ala Ser Gly Lys Lys Ile Pro Leu Ile Phe Gly Glu Arg Arg Pro
225 230 235 240

Gly Asp Ala Glu Ile Leu Phe Ser Glu Thr Thr Lys Ala Glu Arg Glu
245 250 255

Leu Asn Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln
260 265 270

Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Gly Ser Pro Asp Ser
275 280 285

Ile Lys Gln Asn Gly His Gln Thr Asn Gly Ser Ala Asp Ser Ser Lys
290 295 300

Gln Asn Gly His Arg Thr Asn Gly Ser Thr Asp Ser Pro Lys Arg Asn
305 310 315 320

Gly His His Ala Tyr Gly Ser Ala Asp Ser Pro Lys Arg Asn Gly His
325 330 335

Cys Val Phe Gly Ser Ser Asp Leu Lys Pro Asn Gly Asn Gly His Leu
340 345 350

Arg

<210> 19

<211> 1498

<212> DNA

<213> Oryza sativa

<400> 19

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ttgcggacga	tcctgggtgac	ggggcgccgc	ggctacatcg	gcagccacac	cgctctccag	180
ctctctcaac	tcggcttcctg	cgctgtctgtc	ctcgacaacc	tcgacaacgc	ctccgagctc	240
gccatcctcc	cgctcaggga	actcgccgga	cacaacgcga	acaacctcga	cttccgcaag	300
gttgacctcc	gcgacaagca	agcgcttgga	caaatcttct	ctctctcaag	gtttgaggct	360
gtcatccatt	ttgcggggct	gaaagctggt	ggcgagagcg	tgacagaagc	cctgctttac	420
tacgacaaca	acctcatcgg	caccatcact	ctcctgcagg	tcattggcgc	acatggctgc	480
accaagctgg	tggtctcatc	atccgcaact	gtctacgggt	ggcccaagga	ggtgccctgc	540
actgaagaat	ccccactttg	tgcaatgaac	ccctacggga	gaacaaagct	ggtaatcgaa	600
gacatgtgcc	gggatctgca	tgccctcagac	ccaaactgga	agatcatact	gctccgatac	660
ttcaaccctg	ttggagctca	cccaagcggg	tacattgggtg	aggaccctcg	cggcacccca	720
aacaacctca	tgcccttcgt	ccagcaggtc	gctgttgga	ggaggccggc	ccttaccgtc	780
tatggaacgg	actacaacac	caaggatgga	actgggggtc	gtgactatct	ccatgttgtt	840

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gcattcgaga aagcttcttg aaagaaaatc ccgcttgat ttgctggacg aaggcctgga 1020
gatgccgaga tcgtttacgc tcaactgcc aaagctgaga aggaactgaa atggaagcca 1080
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cgcattgta tagggggctt gtaggggtcc agcagcttca tcactagctc ccttaggagg 1380
cctctaatat aatctccata tttatggtag aaataaattt tgcccacggt ggaagaacta 1440
tataatagaa tcatgatgat ttgttgatta aaaaaaaaaa aaaaaaaaaa aaaaaaaa 1498

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<210> 20

<211> 354

<212> PRY

<213> Oryza sativa

<400> 20

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Met Val Ser Ala Leu Leu Arg Thr Ile Leu Val Thr Gly Gly Ala Gly
  1             5             10             15

```

```

Tyr Ile Gly Ser His Thr Val Leu Gln Leu Leu Gln Leu Gly Phe Arg
      20             25             30

```

```

Val Val Val Leu Asp Asn Leu Asp Asn Ala Ser Glu Leu Ala Ile Leu
      35             40             45

```

```

Arg Val Arg Glu Leu Ala Gly His Asn Ala Asn Asn Leu Asp Phe Arg
      50             55             60

```

```

Lys Val Asp Leu Arg Asp Lys Gln Ala Leu Asp Gln Ile Phe Ser Ser
      65             70             75             80

```

```

Gln Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly
      85             90             95

```

```

Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Leu Ile Gly
      100            105            110

```

```

Thr Ile Thr Leu Leu Gln Val Met Ala Ala His Gly Cys Thr Lys Leu
      115            120            125

```

```

Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro
      130            135            140

```

```

Cys Thr Glu Glu Ser Pro Leu Cys Ala Met Asn Pro Tyr Gly Arg Thr
      145            150            155            160

```

```

Lys Leu Val Ile Glu Asp Met Cys Arg Asp Leu His Ala Ser Asp Pro
      165            170            175

```

```

Asn Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His
      180            185            190

```

```

Pro Ser Gly Tyr Ile Gly Glu Asp Pro Cys Gly Ile Pro Asn Asn Leu
      195            200            205

```

```

Met Pro Phe Val Gln Gln Val Ala Val Gly Arg Arg Pro Ala Leu Thr
      210            215            220

```

```

Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly Val Arg Asp

```

225 230 235 240

Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Arg
245 250 255

Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val Tyr Asn Leu
260 265 270

Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu
275 280 285

Lys Ala Ser Gly Lys Lys Ile Pro Leu Val Phe Ala Gly Arg Arg Pro
290 295 300

Gly Asp Ala Glu Ile Val Tyr Ala Gln Thr Ala Lys Ala Glu Lys Glu
305 310 315 320

Leu Lys Trp Trp Lys Ala Lys Tyr Gly Val Glu Glu Met Cys Arg Asp Leu
325 330 335

Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Gly Ser Pro Asp Ser
340 345 350

Ser Asn

<210> 21
<211> 1532
<212> DNA
<213> Glycine max

<400> 21

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tcctctcact	ttcgctcacc	acttaagatt	tccaacaacc	cctctctgca	aaacgcttcg	180
cataagggtac	ttatgcgcca	taagactgta	ctggtaaccg	cgggagccgg	ttacatcgccg	240
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gaaaattcct	ccgaggttgc	catccacaga	gtcagggagc	tcgccggcca	atttgggaac	360
aacctctcct	ttcacaaagt	ggacctacgg	gacagagctg	ctctagacca	aatattttct	420
tcacacacaa	tcgatgctgt	catacatctt	gctggactga	aagcagtagg	agaaaagtgtg	480
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atggctgccc	atggatgcaa	gaagctcggt	ttttcatctt	cagcaactgt	atatggttgg	600
ccaaaggagg	ttccatgcac	agaagagttc	ccctctgtcag	caatgaaccc	atatgggacga	660
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gatcctcggt	gaattccaaa	caatctcatg	ccatttgttc	agcaagtagc	agttggccga	840
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gattacattc	atgttgttga	tttagcagat	gggcacattg	ctgcattgct	taaactagat	960
gaaccttaat	taggttgtga	ggtttataac	ctgggaacag	gaaaggaac	atcagttttg	1020
gagatgggta	gagcttttga	aatggcatct	ggaaagaaaa	ttccacttgt	gatggctggc	1080
ctgtagacctg	gtgatgctga	aatgtgttat	gcatacaaaa	agaaagcgga	aagagagctt	1140
aaatggaaagg	caaaaatatg	catgtgatga	atgtgcctgt	atcaatggaa	ttgggctgaa	1200
aaaaacccct	atggctatgg	agatcagggc	tccaccgatt	aaccacttag	ttttctcttt	1260
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tagttacata	gtaagttaag	agtggtttcc	tatactgtaa	tttaaagggt	ctctaggttc	1440
cttcttacag	gttattgatt	attagattcg	gattctctca	tgttccacat	gagcagcatc	1500
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<210> 22
<211> 349

<212> PRT

<213> Glycine max

<400> 22

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Met Arg Asp Lys Thr Val Leu Val Thr Gly Gly Ala Gly Tyr Ile Gly
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Ser His Thr Val Leu Gln Leu Leu Leu Gly Gly Phe Arg Ala Val Val
      20             25             30

Leu Asp Asn Leu Glu Asn Ser Ser Ser Glu Val Ala Ile His Arg Val Arg
      35             40             45

Glu Leu Ala Gly Glu Phe Gly Asn Asn Leu Ser Phe His Lys Val Asp
      50             55             60

Leu Arg Asp Arg Ala Ala Leu Asp Gln Ile Phe Ser Ser Thr Gln Phe
      65             70             75             80

Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val
      85             90             95

Gln Lys Pro Leu Leu Tyr Tyr Asn Asn Asn Leu Thr Gly Thr Ile Thr
      100            105            110

Leu Leu Glu Val Met Ala Ala His Gly Cys Lys Lys Leu Val Phe Ser
      115            120            125

Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro Cys Thr Glu
      130            135            140

Glu Phe Pro Leu Ser Ala Met Asn Pro Tyr Gly Arg Thr Lys Leu Ile
      145            150            155            160

Ile Glu Glu Ile Cys Arg Asp Val His Cys Ala Glu Pro Asp Cys Lys
      165            170            175

Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro Ser Gly
      180            185            190

Tyr Ile Gly Glu Asp Pro Arg Gly Ile Pro Asn Asn Leu Met Pro Phe
      195            200            205

Val Gln Gln Val Ala Val Gly Arg Arg Pro Ala Leu Thr Val Phe Gly
      210            215            220

Asn Asp Tyr Asn Thr Ser Asp Gly Thr Gly Val Arg Asp Tyr Ile His
      225            230            235            240

Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Leu Lys Leu Asp
      245            250            255

Glu Pro Asn Ile Gly Cys Glu Val Tyr Asn Leu Gly Thr Gly Lys Gly
      260            265            270

Thr Ser Val Leu Glu Met Val Arg Ala Phe Glu Met Ala Ser Gly Lys
      275            280            285

Lys Ile Pro Leu Val Met Ala Gly Arg Arg Pro Gly Asp Ala Glu Ile
      290            295            300

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Val Tyr Ala Ser Thr Lys Lys Ala Glu Arg Glu Leu Lys Trp Lys Ala
 305 310 315 320

Lys Tyr Gly Ile Asp Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Ser
 325 330 335

Lys Asn Pro Tyr Gly Tyr Gly Asp Gln Gly Ser Thr Asp
 340 345

<210> 23
 <211> 490
 <212> DNA
 <213> Triticum aestivum

<220>
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 <221> unsure
 <222> (480)
 <223> n = A, C, G, OR T

<220>
 <221> unsure
 <222> (482)
 <223> n = A, C, G, OR T

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 ttccgcgtcc tegttagtga cagcctcgac aacgcctccg aggaggccat ccgccgcgtc 180
 cgacaactcg ccaacgcccc gcaaaaanagc ctgcacttec gcaagggtga ccttcgtgac 240
 aaggangcgc tgcaccaaat cttctcctcc caaaggatcc ttcnactttt ttccgcaaaa 300
 aagaagtatc ttttttcgng cttattatta anaattaact atagtatatt attgagtcca 360
 caaattaaat gttgatttntt ccgtccgtcc cggccgtcgt gccagccanc canccgntnc 420
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 <212> PRT
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 Leu Gln Gly Phe Arg Val Leu Val Val Asp Ser Leu Asp Asn Ala Ser
 20 25 30
 Glu Glu Ala Ile Arg Arg Val Arg Gln Leu Ala Asn Ala Pro Gln Xaa
 35 40 45
 Ser Leu Asp Phe Arg Lys Val Asp Leu Arg Asp Lys Xaa Ala Leu Asp
 50 55 60
 Gln Ile Phe Ser Ser Gln Arg Tyr Leu Xaa Leu Phe Ser Ala Lys Lys
 65 70 75 80
 Lys Tyr Leu Phe Ser Xaa Leu Leu Leu Xaa Ile Asn Tyr Ser Ile Leu
 85 90 95
 Leu Ser Pro Gln Ile Lys Cys
 100

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 <213> Pisum sativum

<400> 25
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 1 5 10 15
 Ile Gly Thr His Thr Val Val Gln Leu Leu Asn Asn Gly Phe Asn Val
 20 25 30

Ser Ile Ile Asp Asn Phe Asp Asn Ser Val Met Glu Ala Val Glu Arg
 35 40 45
 Val Arg Glu Val Val Gly Ser Asn Leu Ser Gln Asn Leu Glu Phe Thr
 50 55 60
 Leu Gly Asp Leu Arg Asn Lys Asp Asp Leu Glu Lys Leu Phe Ser Lys
 65 70 75 80
 Ser Lys Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly
 85 90 95
 Glu Ser Val Glu Asn Pro Arg Arg Tyr Phe Asp Asn Asn Leu Val Gly
 100 105 110
 Thr Ile Asn Leu Tyr Glu Val Met Ala Lys His Asn Cys Lys Lys Met
 115 120 125
 Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Lys Ile Pro
 130 135 140
 Cys Val Glu Asp Phe Lys Leu Gln Ala Met Asn Pro Tyr Gly Arg Thr
 145 150 155 160
 Lys Leu Phe Leu Glu Glu Ile Ala Arg Asp Ile Gln Lys Ala Glu Pro
 165 170 175
 Glu Trp Arg Ile Val Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His
 180 185 190
 Glu Ser Gly Lys Leu Gly Glu Asp Pro Arg Gly Ile Pro Asn Asn Leu
 195 200 205
 Met Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn
 210 215 220
 Val Tyr Gly His Asp Tyr Pro Thr Arg Asp Gly Ser Ala Ile Arg Asp
 225 230 235 240
 Tyr Ile His Val Met Asp Leu Ala Asp Gly His Ile Ala Ala Leu Arg
 245 250 255
 Lys Leu Phe Thr Ser Glu Asn Ile Gly Cys Thr Ala Tyr Asn Leu Gly
 260 265 270
 Thr Gly Arg Gly Ser Ser Val Leu Glu Met Val Ala Ala Phe Glu Lys
 275 280 285
 Ala Ser Gly Lys Lys Ile Ala Leu Lys Leu Cys Pro Arg Arg Pro Gly
 290 295 300
 Asp Ala Thr Glu Val Tyr Ala Ser Thr Ala Lys Ala Glu Lys Glu Leu
 305 310 315 320
 Gly Trp Lys Ala Lys Tyr Gly Val Glu Glu Met Cys Arg Asp Gln Trp
 325 330 335
 Asn Trp Ala Lys Asn Asn Pro Trp Gly Tyr Ser Gly Lys Pro
 340 345 350

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 <211> 350
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 <213> Cyamopsis tetragonoloba

<400> 26

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Met Ser Ser Gln Thr Val Leu Val Thr Gly Gly Ala Gly Tyr Ile Gly
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Ser His Thr Val Leu Gln Leu Leu Leu Gly Gly Phe Lys Ala Val Val
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Val Asp Asn Leu Asp Asn Ser Ser Glu Thr Ala Ile His Arg Val Lys
      35              40              45

Glu Leu Ala Gly Lys Phe Ala Gly Asn Leu Ser Phe His Lys Leu Asp
 50              55              60

Leu Arg Asp Arg Asp Ala Leu Glu Lys Ile Phe Ser Ser Thr Lys Phe
 65              70              75              80

Asp Ser Val Ile His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val
      85              90              95

Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Leu Ile Gly Thr Ile Val
      100              105              110

Leu Phe Glu Val Met Ala Ala His Gly Cys Lys Lys Leu Val Phe Ser
 115              120              125

Ser Ser Ala Thr Val Tyr Gly Leu Pro Lys Glu Val Pro Cys Thr Glu
 130              135              140

Glu Phe Pro Leu Ser Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile
 145              150              155              160

Ile Glu Glu Ile Cys Arg Asp Ile Tyr Arg Ala Glu Gln Glu Trp Lys
      165              170              175

Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His Pro Ser Gly
 180              185              190

Tyr Ile Gly Glu Asp Pro Arg Gly Ile Pro Asn Asn Leu Met Pro Phe
      195              200              205

Val Gln Gln Val Ala Val Gly Arg Arg Pro Ala Leu Thr Val Phe Gly
 210              215              220

Asn Asp Tyr Thr Thr Ser Asp Gly Thr Gly Val Arg Asp Tyr Ile His
 225              230              235              240

Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Arg Lys Leu Asn
      245              250              255

Asp Pro Lys Ile Gly Cys Glu Val Tyr Asn Leu Gly Thr Gly Lys Gly
 260              265              270

Thr Ser Val Leu Glu Met Val Lys Ala Phe Glu Gln Ala Ser Gly Lys
 275              280              285

Lys Ile Pro Leu Val Met Ala Gly Arg Arg Pro Gly Asp Ala Glu Val

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290

295

300

Val Tyr Ala Ser Thr Asn Lys Ala Glu Arg Glu Leu Asn Trp Lys Ala
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Lys Tyr Gly Ile Asp Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Ser
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Lys Asn Pro Tyr Gly Tyr Gly Gly Ser Glu Asp Ser Ser Asn
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ctgtctctc

9